

<120> COMPOSITIONS AND METHODS FOR IMPROVING
KIDNEY FUNCTION

<130> 00-100

<150> US 60/244,479

<151> 2000-10-30

<160> 10

<170> FastSEQ for Windows Version 3.0

 $\langle 210 \rangle$ 1

<211> 1882

<212> DNA

<213> Homo sapiens

 $\langle 220 \rangle$

<221> CDS

<222> (226)...(1338)

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cagggcgagc	gcaggcggcg	agagcgcagg	gcggcgcgcc	gtcgggtccc	ggagcagaac	180
ccggcctttt	cttgagcgca	cgctgtctct	agtcgctgat	cccaa atg	cac cggtctc	237

Met His Arg Leu

1

atc ttt gtc tac act cta atc tgc gca aac ttt tgc agc tgt cgg gac 285
Ile Phe Val Tyr Thr Leu Ile Cys Ala Asn Phe Cys Ser Cys Arg Asp
5 10 15 20

act tct gca acc ccg cag agc gca tcc atc aaa gct ttg cgc aac gcc 333
Thr Ser Ala Thr Pro Gln Ser Ala Ser Ile Lys Ala Leu Arg Asn Ala
25 30 35

aac ctc agg cga gat gag agc aat cac ctc aca gac ttg tac cga aga Asn Leu Arg Arg Asp Glu Ser Asn His Leu Thr Asp Leu Tyr Arg Arg	381
40 45 50	
gat gag acc atc cag gtg aaa gga aac ggc tac gtg cag agt cct aga Asp Glu Thr Ile Gln Val Lys Gly Asn Gly Tyr Val Gln Ser Pro Arg	429
55 60 65	
ttc ccg aac agc tac ccc agg aac ctg ctc ctg aca tgg cgg ctt cac Phe Pro Asn Ser Tyr Pro Arg Asn Leu Leu Leu Thr Trp Arg Leu His	477
70 75 80	
tct cag gag aat aca cgg ata cag cta gtg ttt gac aat cag ttt gga Ser Gln Glu Asn Thr Arg Ile Gln Leu Val Phe Asp Asn Gln Phe Gly	525
85 90 95 100	
tta gag gaa gca gaa aat gat atc tgt agg tat gat ttt gtg gaa gtt Leu Glu Glu Ala Glu Asn Asp Ile Cys Arg Tyr Asp Phe Val Glu Val	573
105 110 115	
gaa gat ata tcc gaa acc agt acc att att aga gga cga tgg tgt gga Glu Asp Ile Ser Glu Thr Ser Thr Ile Ile Arg Gly Arg Trp Cys Gly	621
120 125 130	
cac aag gaa gtt cct cca agg ata aaa tca aga acg aac caa att aaa His Lys Glu Val Pro Pro Arg Ile Lys Ser Arg Thr Asn Gln Ile Lys	669
135 140 145	
atc aca ttc aag tcc gat gac tac ttt gtg gct aaa cct gga ttc aag Ile Thr Phe Lys Ser Asp Asp Tyr Phe Val Ala Lys Pro Gly Phe Lys	717
150 155 160	
att tat tat tct ttg ctg gaa gat ttc caa ccc gca gca gct tca gag Ile Tyr Tyr Ser Leu Leu Glu Asp Phe Gln Pro Ala Ala Ala Ser Glu	765
165 170 175 180	
acc aac tgg gaa tct gtc aca agc tct att tca ggg gta tcc tat aac Thr Asn Trp Glu Ser Val Thr Ser Ser Ile Ser Gly Val Ser Tyr Asn	813
185 190 195	
tct cca tca gta acg gat ccc act ctg att gcg gat gct ctg gac aaa Ser Pro Ser Val Thr Asp Pro Thr Leu Ile Ala Asp Ala Leu Asp Lys	861
200 205 210	

aaa att gca gaa ttt gat aca gtg gaa gat ctg ctc aag tac ttc aat 909
 Lys Ile Ala Glu Phe Asp Thr Val Glu Asp Leu Leu Lys Tyr Phe Asn
 215 220 225

cca gag tca tgg caa gaa gat ctt gag aat atg tat ctg gac acc cct 957
 Pro Glu Ser Trp Gln Glu Asp Leu Glu Asn Met Tyr Leu Asp Thr Pro
 230 235 240

cgg tat cga ggc agg tca tac cat gac cgg aag tca aaa gtt gac ctg 1005
 Arg Tyr Arg Gly Arg Ser Tyr His Asp Arg Lys Ser Lys Val Asp Leu
 245 250 255 260

gat agg ctc aat gat gat gcc aag cgt tac agt tgc act ccc agg aat 1053
 Asp Arg Leu Asn Asp Asp Ala Lys Arg Tyr Ser Cys Thr Pro Arg Asn
 265 270 275

tac tcg gtc aat ata aga gaa gag ctg aag ttg gcc aat gtg gtc ttc 1101
 Tyr Ser Val Asn Ile Arg Glu Glu Leu Lys Leu Ala Asn Val Val Phe
 280 285 290

ttt cca cgt tgc ctc ctc gtg cag cgc tgt gga gga aat tgt ggc tgt 1149
 Phe Pro Arg Cys Leu Leu Val Gln Arg Cys Gly Gly Asn Cys Gly Cys
 295 300 305

gga act gtc aac tgg agg tcc tgc aca tgc aat tca ggg aaa acc gtg 1197
 Gly Thr Val Asn Trp Arg Ser Cys Thr Cys Asn Ser Gly Lys Thr Val
 310 315 320

aaa aag tat cat gag gta tta cag ttt gag cct ggc cac atc aag agg 1245
 Lys Lys Tyr His Glu Val Leu Gln Phe Glu Pro Gly His Ile Lys Arg
 325 330 335 340

agg ggt aga gct aag acc atg gct cta gtt gac atc cag ttg gat cac 1293
 Arg Gly Arg Ala Lys Thr Met Ala Leu Val Asp Ile Gln Leu Asp His
 345 350 355

cat gaa cga tgc gat tgt atc tgc agc tca aga cca cct cga taa 1338
 His Glu Arg Cys Asp Cys Ile Cys Ser Ser Arg Pro Pro Arg *
 360 365 370

gagaatgtgc acatccttac attaagcctg aaagaacctt tagtttaagg aggggtgagat 1398

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aagagaccct tttcctacca gcaaccaaac ttactactag cctgcaatgc aatgaacaca 1458
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tcaacttcta tacctaagaa tataggattg catttaataa tagtgtttga ggttatatat 1578
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ttttggtata tataaccagg tacaccagag gttacatatg tttgagttag actcttaaaa 1698
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<210> 2

<211> 370

<212> PRT

<213> Homo sapiens

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Leu Arg Asn Ala Asn Leu Arg Arg Asp Glu Ser Asn His Leu Thr Asp
35          40          45
Leu Tyr Arg Arg Asp Glu Thr Ile Gln Val Lys Gly Asn Gly Tyr Val
50          55          60
Gln Ser Pro Arg Phe Pro Asn Ser Tyr Pro Arg Asn Leu Leu Leu Thr
65          70          75          80
Trp Arg Leu His Ser Gln Glu Asn Thr Arg Ile Gln Leu Val Phe Asp
85          90          95
Asn Gln Phe Gly Leu Glu Glu Ala Glu Asn Asp Ile Cys Arg Tyr Asp
100         105         110
Phe Val Glu Val Glu Asp Ile Ser Glu Thr Ser Thr Ile Ile Arg Gly
115         120         125
Arg Trp Cys Gly His Lys Glu Val Pro Pro Arg Ile Lys Ser Arg Thr
130         135         140
Asn Gln Ile Lys Ile Thr Phe Lys Ser Asp Asp Tyr Phe Val Ala Lys
145         150         155         160
Pro Gly Phe Lys Ile Tyr Tyr Ser Leu Leu Glu Asp Phe Gln Pro Ala
165         170         175
Ala Ala Ser Glu Thr Asn Trp Glu Ser Val Thr Ser Ser Ile Ser Gly
180         185         190
Val Ser Tyr Asn Ser Pro Ser Val Thr Asp Pro Thr Leu Ile Ala Asp
195         200         205

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Ala Leu Asp Lys Lys Ile Ala Glu Phe Asp Thr Val Glu Asp Leu Leu
 210 215 220
 Lys Tyr Phe Asn Pro Glu Ser Trp Gln Glu Asp Leu Glu Asn Met Tyr
 225 230 235 240
 Leu Asp Thr Pro Arg Tyr Arg Gly Arg Ser Tyr His Asp Arg Lys Ser
 245 250 255
 Lys Val Asp Leu Asp Arg Leu Asn Asp Asp Ala Lys Arg Tyr Ser Cys
 260 265 270
 Thr Pro Arg Asn Tyr Ser Val Asn Ile Arg Glu Glu Leu Lys Leu Ala
 275 280 285
 Asn Val Val Phe Phe Pro Arg Cys Leu Leu Val Gln Arg Cys Gly Gly
 290 295 300
 Asn Cys Gly Cys Gly Thr Val Asn Trp Arg Ser Cys Thr Cys Asn Ser
 305 310 315 320
 Gly Lys Thr Val Lys Lys Tyr His Glu Val Leu Gln Phe Glu Pro Gly
 325 330 335
 His Ile Lys Arg Arg Gly Arg Ala Lys Thr Met Ala Leu Val Asp Ile
 340 345 350
 Gln Leu Asp His His Glu Arg Cys Asp Cys Ile Cys Ser Ser Arg Pro
 355 360 365
 Pro Arg
 370

<210> 3
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<220>
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 <222> (93)...(1205)

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 Met Gln Arg Leu Val Leu Val
 1 5
 tcc att ctc ctg tgc gcg aac ttt agc tgc tat ccg gac act ttt gcg 161
 Ser Ile Leu Leu Cys Ala Asn Phe Ser Cys Tyr Pro Asp Thr Phe Ala
 10 15 20

act ccg cag aga gca tcc atc aaa gct ttg cgc aat gcc aac ctc agg	209
Thr Pro Gln Arg Ala Ser Ile Lys Ala Leu Arg Asn Ala Asn Leu Arg	
25 30 35	
aga gat gag agc aat cac ctc aca gac ttg tac cag aga gag gag aac	257
Arg Asp Glu Ser Asn His Leu Thr Asp Leu Tyr Gln Arg Glu Glu Asn	
40 45 50 55	
att cag gtg aca agc aat ggc cat gtg cag agt cct cgc ttc ccg aac	305
Ile Gln Val Thr Ser Asn Gly His Val Gln Ser Pro Arg Phe Pro Asn	
60 65 70	
agc tac cca agg aac ctg ctt ctg aca tgg tgg ctc cgt tcc cag gag	353
Ser Tyr Pro Arg Asn Leu Leu Leu Thr Trp Trp Leu Arg Ser Gln Glu	
75 80 85	
aaa aca cgg ata caa ctg tcc ttt gac cat caa ttc gga cta gag gaa	401
Lys Thr Arg Ile Gln Leu Ser Phe Asp His Gln Phe Gly Leu Glu Glu	
90 95 100	
gca gaa aat gac att tgt agg tat gac ttt gtg gaa gtt gaa gaa gtc	449
Ala Glu Asn Asp Ile Cys Arg Tyr Asp Phe Val Glu Val Glu Glu Val	
105 110 115	
tca gag agc agc act gtt gtc aga gga aga tgg tgt ggc cac aag gag	497
Ser Glu Ser Ser Thr Val Val Arg Gly Arg Trp Cys Gly His Lys Glu	
120 125 130 135	
atc cct cca agg ata acg tca aga aca aac cag att aaa atc aca ttt	545
Ile Pro Pro Arg Ile Thr Ser Arg Thr Asn Gln Ile Lys Ile Thr Phe	
140 145 150	
aag tct gat gac tac ttt gtg gca aaa cct gga ttc aag att tat tat	593
Lys Ser Asp Asp Tyr Phe Val Ala Lys Pro Gly Phe Lys Ile Tyr Tyr	
155 160 165	
tca ttt gtg gaa gat ttc caa ccg gaa gca gcc tca gag acc aac tgg	641
Ser Phe Val Glu Asp Phe Gln Pro Glu Ala Ala Ser Glu Thr Asn Trp	
170 175 180	
gaa tca gtc aca agc tct ttc tct ggg gtg tcc tat cac tct cca tca	689
Glu Ser Val Thr Ser Ser Phe Ser Gly Val Ser Tyr His Ser Pro Ser	
185 190 195	

ata acg gac ccc act ctc act gct gat gcc ctg gac aaa act gtc gca Ile Thr Asp Pro Thr Leu Thr Ala Asp Ala Leu Asp Lys Thr Val Ala 200 205 210 215	737
gaa ttc gat acc gtg gaa gat cta ctt aag cac ttc aat cca gtg tct Glu Phe Asp Thr Val Glu Asp Leu Leu Lys His Phe Asn Pro Val Ser 220 225 230	785
tgg caa gat gat ctg gag aat ttg tat ctg gac acc cct cat tat aga Trp Gln Asp Asp Leu Glu Asn Leu Tyr Leu Asp Thr Pro His Tyr Arg 235 240 245	833
ggc agg tca tac cat gat cgg aag tcc aaa gtg gac ctg gac agg ctc Gly Arg Ser Tyr His Asp Arg Lys Ser Lys Val Asp Leu Asp Arg Leu 250 255 260	881
aat gat gat gtc aag cgt tac agt tgc act ccc agg aat cac tct gtg Asn Asp Asp Val Lys Arg Tyr Ser Cys Thr Pro Arg Asn His Ser Val 265 270 275	929
aac ctc agg gag gag ctg aag ctg acc aat gca gtc ttc ttc cca cga Asn Leu Arg Glu Glu Leu Lys Leu Thr Asn Ala Val Phe Phe Pro Arg 280 285 290 295	977
tgc ctc ctc gtg cag cgc tgt ggt ggc aac tgt ggt tgc gga act gtc Cys Leu Leu Val Gln Arg Cys Gly Gly Asn Cys Gly Cys Gly Thr Val 300 305 310	1025
aac tgg aag tcc tgc aca tgc agc tca ggg aag aca gtg aag aag tat Asn Trp Lys Ser Cys Thr Cys Ser Ser Gly Lys Thr Val Lys Lys Tyr 315 320 325	1073
cat gag gta ttg aag ttt gag cct gga cat ttc aag aga agg ggc aaa His Glu Val Leu Lys Phe Glu Pro Gly His Phe Lys Arg Arg Gly Lys 330 335 340	1121
gct aag aat atg gct ctt gtt gat atc cag ctg gat cat cat gag cga Ala Lys Asn Met Ala Leu Val Asp Ile Gln Leu Asp His His Glu Arg 345 350 355	1169

tgt gac tgt atc tgc agc tca aga cca cct cga taa aacactatgc 1215
 Cys Asp Cys Ile Cys Ser Ser Arg Pro Pro Arg *
 360 365 370

acatctgtac ttgattatg aaaggacctt taggttacaa aaaccctaag aagcttctaa 1275
 tctcagtga atgaatgcat atggaaatgt tgctttgtta gtgcatggc aagaagaagc 1335
 aaatatcatt aatttctata tacataaaca taggaattca cttatcaata gtatgtgaag 1395
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 attcagtata ttactg 1472

<210> 4

<211> 370

<212> PRT

<213> Mus musculus

<400> 4

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 20 25 30
 Leu Arg Asn Ala Asn Leu Arg Arg Asp Glu Ser Asn His Leu Thr Asp
 35 40 45
 Leu Tyr Gln Arg Glu Glu Asn Ile Gln Val Thr Ser Asn Gly His Val
 50 55 60
 Gln Ser Pro Arg Phe Pro Asn Ser Tyr Pro Arg Asn Leu Leu Leu Thr
 65 70 75 80
 Trp Trp Leu Arg Ser Gln Glu Lys Thr Arg Ile Gln Leu Ser Phe Asp
 85 90 95
 His Gln Phe Gly Leu Glu Glu Ala Glu Asn Asp Ile Cys Arg Tyr Asp
 100 105 110
 Phe Val Glu Val Glu Glu Val Ser Glu Ser Ser Thr Val Val Arg Gly
 115 120 125
 Arg Trp Cys Gly His Lys Glu Ile Pro Pro Arg Ile Thr Ser Arg Thr
 130 135 140
 Asn Gln Ile Lys Ile Thr Phe Lys Ser Asp Asp Tyr Phe Val Ala Lys
 145 150 155 160
 Pro Gly Phe Lys Ile Tyr Tyr Ser Phe Val Glu Asp Phe Gln Pro Glu
 165 170 175
 Ala Ala Ser Glu Thr Asn Trp Glu Ser Val Thr Ser Ser Phe Ser Gly
 180 185 190
 Val Ser Tyr His Ser Pro Ser Ile Thr Asp Pro Thr Leu Thr Ala Asp
 195 200 205

Ala Leu Asp Lys Thr Val Ala Glu Phe Asp Thr Val Glu Asp Leu Leu
 210 215 220
 Lys His Phe Asn Pro Val Ser Trp Gln Asp Asp Leu Glu Asn Leu Tyr
 225 230 235 240
 Leu Asp Thr Pro His Tyr Arg Gly Arg Ser Tyr His Asp Arg Lys Ser
 245 250 255
 Lys Val Asp Leu Asp Arg Leu Asn Asp Asp Val Lys Arg Tyr Ser Cys
 260 265 270
 Thr Pro Arg Asn His Ser Val Asn Leu Arg Glu Glu Leu Lys Leu Thr
 275 280 285
 Asn Ala Val Phe Phe Pro Arg Cys Leu Leu Val Gln Arg Cys Gly Gly
 290 295 300
 Asn Cys Gly Cys Gly Thr Val Asn Trp Lys Ser Cys Thr Cys Ser Ser
 305 310 315 320
 Gly Lys Thr Val Lys Lys Tyr His Glu Val Leu Lys Phe Glu Pro Gly
 325 330 335
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 Gln Leu Asp His His Glu Arg Cys Asp Cys Ile Cys Ser Ser Arg Pro
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 Pro Arg
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<212> DNA

<213> Artificial Sequence

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<210> 6

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5

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